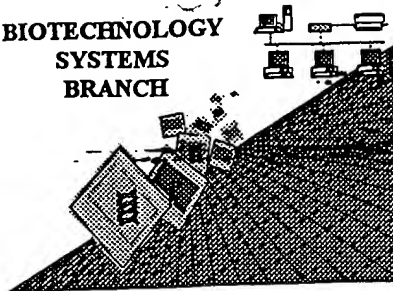


Hunt

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



2112

**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/506,079 A

Source: 1642

Date Processed by STIC: 9-28-00

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TECH CENTER 1600 1900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

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# Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/506,079A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

*1-Hunt*

1642

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/506,079A DATE: 09/28/2000  
TIME: 11:04:01

Input Set : A:\SEQUENCE.txt  
Output Set: N:\CRF3\09282000\I506079A.raw

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:  
C--> 4 (i) APPLICANT: Clinton, Gail M., Doherty, Joni Kristin, and Adelman, John P.  
6 (ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS  
8 (iii) NUMBER OF SEQUENCES: 10  
10 (iv) CORRESPONDENCE ADDRESS:  
11 (A) ADDRESSEE: DAVIS WRIGHT TREMAINE  
12 (B) STREET: 1501 Fourth Avenue, 2600 Century Square  
13 (C) CITY: Seattle  
14 (D) STATE: Washington  
15 (E) COUNTRY: U.S.A.  
16 (F) ZIP: 98101  
18 (v) COMPUTER READABLE FORM:  
19 (A) MEDIUM TYPE: Floppy disk  
20 (B) COMPUTER: PC compatible  
21 (C) OPERATING SYSTEM: Windows95  
22 (D) SOFTWARE: Word  
24 (vi) CURRENT APPLICATION DATA:  
C--> 25 (A) APPLICATION NUMBER: US/09/506,079A  
C--> 26 (B) FILING DATE: 16-Feb-2000  
27 (C) CLASSIFICATION:  
29 (viii) ATTORNEY/AGENT INFORMATION:  
30 (A) NAME: Oster, Jeffrey B.  
31 (B) REGISTRATION NUMBER: 32,585  
32 (C) REFERENCE/DOCKET NUMBER: 49321-1  
34 (ix) TELECOMMUNICATION INFORMATION:  
35 (A) TELEPHONE: 206 628 7711  
36 (B) TELEFAX: 206 628 7699

Does Not Comply  
Corrected Diskette Needed

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ERRORED SEQUENCES

59 (2) INFORMATION FOR SEQ ID NO: 2:  
61 (i) SEQUENCE CHARACTERISTICS:  
62 (A) LENGTH: 418  
63 (B) TYPE: amino acid  
64 (C) STRANDEDNESS: single  
65 (D) TOPOLOGY: unknown  
66 (ii) MOLECULE TYPE: polypeptide  
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
69 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Ala Leu Leu  
70 5 10 15  
71 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys  
E--> 72 20 25 30  
73 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
E--> 74 35 40 45  
75 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
50 55 60

*see bottom of next page*

*} misaligned  
amino acid  
numbering. see  
#4 on Error*

*Summary  
Sheet*

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/506,079A

DATE: 09/28/2000

TIME: 11:04:01

Input Set : A:\SEQUENCE.txt

Output Set: N:\CRF3\09282000\I506079A.raw

```

E--> 76      50      55      60
      77 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
E--> 78 65 68      70 78      75 78      80
      79 Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu
E--> 80 80      85      90      95
      81 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
E--> 82      100      105      110
      83 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Arg Arg Thr Thr Pro
E--> 84      115      120      125
      85 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
E--> 86      130      135      140
      87 Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
E--> 88      145      150      155
      89 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
E--> 90 160      165      170      175
      91 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
E--> 92      180      185      190
      93 His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
E--> 94      195      200      205
      95 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
E--> 96      210      215      220
      97 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
E--> 98      225      230      235
      99 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
E--> 100 240      245      250      255
      101 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
E--> 102      260      265      270
      103 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
E--> 104      275      280      285
      105 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
E--> 106      290      295      300
      107 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
E--> 108      305      310      315
      109 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
E--> 110 320      325      330      335
W--> 111 Pro Cys Ala Arg Val Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala
E--> 112      340      345      350
W--> 113 Val Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu
E--> 114      355      360      365
W--> 115 Ser Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu
E--> 116      370      375      380
W--> 117 Pro Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser
E--> 118      385      390      395
W--> 119 Val Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
E--> 120 400      405      410      415
E--> 121 Arg Tyr Glu (Gly)

```

*Misaligned  
amino  
acid  
numbering*

*420 amino acids shown  
418 listed as length*

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**OCT 13 2000**

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VERIFICATION SUMMARY                      DATE: 09/28/2000  
PATENT APPLICATION:    US/09/506,079A              TIME: 11:04:02

Input Set : A:\SEQUENCE.txt  
Output Set: N:\CRF3\09282000\I506079A.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]  
L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:45 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1, Value=[HER-2 ECD antagonist]  
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:72 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:121 M:203 E: No. of Seq. differs, LENGTH:Input:418 Found:420 SEQ:2  
L:130 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[oligonucleotide]  
L:142 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4, Value=[oligonucleotide]  
L:153 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[oligonucleotide]  
L:165 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=[oligonucleotide]  
L:176 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[oligonucleotide]  
L:187 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8, Value=[oligonucleotide]  
L:198 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9, Value=[oligonucleotide]  
L:209 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10, Value=[DNA]  
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

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